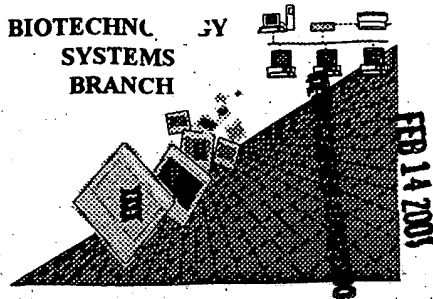


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BIOTECHNOLOGY
SYSTEMS
BRANCH



RECEIVED

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

#13

Application Serial Number:

09/145,916A

Source:

1636

Date Processed by STIC:

2/5/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/145,916A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 J Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
 Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
 file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
 Instead, please use "File Manager" or any other means to copy file to floppy disk.

1636

RAW SEQUENCE LISTING DATE: 02/05/2001
 PATENT APPLICATION: US/09/145,916A TIME: 14:45:59

Input Set : A:\ES.txt
 Output Set: N:\CRF3\02052001\I145916A.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:
 2 (i) APPLICANT: Simons, Michael
 3 Volk, Rudiger
 4 Horowitz, Arie
 5 (ii) TITLE OF INVENTION: Stimulation of angiogenesis
 6 via enhanced endothelial expression of syndecan-4
 7 core proteins
 8 (iii) NUMBER OF SEQUENCES: 23
 9 (iv) CORRESPONDENCE ADDRESS:
 10 (A) ADDRESSEE: David Prashker, Esq.
 11 (B) STREET: P.O. Box 5387
 12 (C) CITY: Magnolia
 13 (D) STATE: Massachusetts
 14 (E) COUNTRY: USA
 15 (F) ZIP: 01930
 16 (v) COMPUTER READABLE FORM:
 17 (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
 18 (B) COMPUTER: Dell PC
 19 (C) OPERATING SYSTEM: MS DOS
 20 (D) SOFTWARE: Microsoft Word version 97
 21 (vi) CURRENT APPLICATION DATA:
 22 (A) APPLICATION NUMBER: US/09/145,916A
 23 (B) FILING DATE: 02-Sep-1998
 24 (C) CLASSIFICATION: Unknown
 25 (viii) ATTORNEY/AGENT INFORMATION:
 26 (A) NAME: David Prashker, Esq.
 27 (B) REGISTRATION NUMBER: 29,693
 28 (C) REFERENCE/DOCKET NUMBER: BIS-039
 29 (ix) TELECOMMUNICATION INFORMATION:
 30 (A) TELEPHONE: (978) 525-3794

Does Not Comply
 Corrected Diskette Needed:

pg 12

ERRORED SEQUENCES

392 (2) INFORMATION FOR SEQ ID NO: 17:
 393 (i) SEQUENCE CHARACTERISTICS:
 394 (A) LENGTH: 9 amino acids
 395 (B) TYPE: amino acid
 396 (C) STRANDEDNESS: single
 397 (D) TOPOLOGY: linear
 398 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 400 Leu Gly Lys Lys Pro Ile Tyr Lys Lys
 401 1 5 S
 423 (2) INFORMATION FOR SEQ ID NO: 20:
 424 (i) SEQUENCE CHARACTERISTICS:
 425 (A) LENGTH: 33 base pairs

*← misaligned amino acid nos. - see item 4 on
 Erra Summary
 Sheet*

RAW SEQUENCE LISTING

DATE: 02/05/2001

PATENT APPLICATION: US/09/145,916A

TIME: 14:45:59

Input Set : A:\ES.txt

Output Set: N:\CRF3\02052001\I145916A.raw

426 (B) TYPE: nucleic acid
427 (C) STRANDEDNESS: single
428 (D) TOPOLOGY: linear
429 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

E--> 431 ATAGAGCTCT TGGGAACCATG G⁰CTGTCT GCC

33

invalid nucleotide designator

VERIFICATION SUMMARY

DATE: 02/05/2001

PATENT APPLICATION: US/09/145,916A

TIME: 14:46:00

Input Set : A:\ES.txt

Output Set: N:\CRF3\02052001\I145916A.raw

L:22 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:23 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:401 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ TD:17
L:431 M:320 E: (1) Wrong Nucleic Acid Designator, 1